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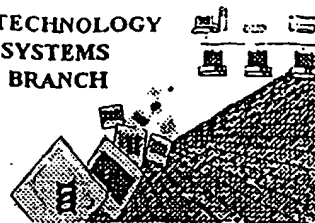
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RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/798,096

Source: EFWD

Date Processed by STIC: 3/22/04

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT

MARK SPENCER, TELEPHONE: 703-308-4212; FAX: 703-308-4221

Effective 12/13/03: TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE SEE BELOW FOR ADDRESS

<http://www.uspto.gov/web/offices/pac/checker/chkr41note.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses.

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313 1450
3. Hand Carry directly to (EFFECTIVE 12/01/03):
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 10/08/03

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10798,096

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☐ **Wrapped Nucleics
Wrapped Aminos** The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

- 2 ☐ **Invalid Line Length** The rules require that a line not exceed 72 characters in length. This includes white spaces.

- 3 ☐ **Misaligned Amino
Numbering** The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

- 4 ☒ **Non-ASCII** The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

- 5 ☐ **Variable Length** Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

- 6 ☐ **PatentIn 2.0
"bug"** A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s). Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

- 7 ☐ **Skipped Sequences
(OLD RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

- 8 ☐ **Skipped Sequences
(NEW RULES)** Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

- 9 ☐ **Use of n's or Xaa's
(NEW RULES)** Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

- 10 ☐ **Invalid <213>
Response** Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence

- 11 ☐ **Use of <220>** Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)

- 12 ☐ **PatentIn 2.0
"bug"** Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

- 13 ☐ **Misuse of n/Xaa** "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



SEQUENCE LISTING

10/998,096

Page 1

<110> Rea-Min Chu

Ching-Yi Lin

Ya-Wen Hsiao

Kuang-Wen Liao

Submitted file
could not be processed
due to numerous errors

<120> COMPLEX IMMUNO-GENE MEDICAL COMPOSITION FOR INHIBITING TUMOR CELLS

<160>4

<210>1

<211>636

<212> mRNA and PRT

<213> Human

<220> -

<221> IL-6

<300>

<308> NCBI pubmed Genbank ; Accession No. : NM 000600

<309> ← please insert, mandatory, if <308> is shown

<400>1

63 78 93 108
atg aac tcc ttc tcc aca agc gcc ttc ggt cca gtt gcc tcc tcc ctg ggg ctg ctg ctg
Met Asn Ser Phe Ser Thr Ser Ala Phe Gly Pro Val Ala Phe Ser Leu Gly Leu Leu Leu
1 5 10 15 20
123 138 153 168
gtg ttg cct gct gcc ttc cct gcc cca gta ccc cca gga gaa gat tcc aaa gat gta gcc
Val Leu Pro Ala Ala Phe Pro Ala Pro Val Pro Pro Gly Glu Asp Ser Lys Asp Val Ala
25 30 35 40
183 198 213 228
gcc cca cac aga cag cca ctc acc tct tca gaa cga att gac aaa caa att cgg tac atc
Ala Pro His Arg Gln Pro Leu Thr Ser Ser Glu Arg Ile Asp Lys Gln Ile Arg Tyr Ile
45 50 55 60
243 258 273 288
ctc gac ggc atc tca gcc ctg aga aag gag aca tgt aac aag agt aac atg tgt gaa agc
Leu Asp Gly Ile Ser Ala Leu Arg Lys Glu Thr Cys Asn Lys Ser Asn Met Cys Glu Ser
65 70 75 80
303 318 333 348
agc aaa gag gca ctg gca gaa aac aac ctg aac ctt cca aag atg gct gaa aaa gat gga
Ser Lys Glu Ala Leu Ala Glu Asn Asn Leu Asn Leu Pro Lys Met Ala Glu Lys Asp Gly
85 90 95 100
363 378 393 408
tgc ttc caa tct gga ttc aat gag gag act tgc ctg gtg aaa atc atc act ggt ctt ttg
Cys Phe Gln Ser Gly Phe Asn Glu Glu Thr Thr Cys Leu Val Lys Ile Ile Thr Gly Leu Leu
105 110 115 120
423 438 453 468

delete, mandatory, <212> has to be either
DNA, RNA or PRT, if
it is both DNA/RNA
please use type DNA
and explain in section
<220>-<223>

Please insert dates for
each accession No.

60 with resp

← please
see id
4
on er
Summe
Sheet

gag	ttt	gag	gta	tac	cta	cag	tac	ctc	cag	aac	aga	ttt	gag	agt	agt	gag	gaa	caa	gcc	420																																																								
Glu	Phe	Glu	Val	Tyr	Leu	Glu	Tyr	Leu	Gln	Asn	Arg	Phe	Glu	Ser	Ser	Glu	Glu	Gln	Ala	140																																																								
483																			498																			513																			528																			480
aga	gct	gtg	cag	atg	agt	acu	aaa	gfc	ctg	atc	cag	ttc	ctg	cag	aaa	aag	gca	aag	aat	480																																																								
Arg	Ala	Val	Gln	Met	Ser	Thr	Lys	Val	Leu	Ile	Gln	Phe	Leu	Gln	Lys	Lys	Ala	Lys	Asn	160																																																								
543																			558																			573																			588																			540
cta	gat	gca	ata	acc	acc	cct	gac	cca	acc	aca	aat	gcc	agc	ctg	ctg	acg	aag	ctg	cag	540																																																								
Leu	Asp	Ala	Ile	Thr	Thr	Pro	Asp	Pro	Thr	Thr	Asn	Ala	Ser	Leu	Leu	Thr	Lys	Leu	Gln	180																																																								
603																			618																			633																			648																			600
gca	cag	aac	cag	igg	ctg	cag	gac	atg	aca	act	cat	ctc	att	ctg	cgc	agc	ttt	aag	gag	600																																																								
Ala	Gln	Asn	Gln	Trp	Leu	Gln	Asp	Met	Thr	Thr	His	Leu	Ile	Leu	Arg	Ser	Phe	Lys	Glu	200																																																								
663																			678																			693																			636																			
ttc	ctg	cag	tcu	agc	ctg	agg	gct	ctt	cgg	cau	atg											636																																																						
Phe	Leu	Gln	Ser	Ser	Leu	Arg	Ala	Leu	Arg	Gln	Met											636																																																						

delete, see
item #4
on
error
summary
sheet

<210>2

<211>60

<212>

mRNA and PRT

delete

<213>Human

please insert

<221>

IL-2 Signal Peptide

please insert into section <223>

<300>

<308>NCBI pubmed Genbank

(Accession No. : V00564)

-same error

<309>

insert with response

<400>2

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Met	Tyr	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu	Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	20
1				5				10				15				20				

<210>3

<211>342

<212>

mRNA and PRT

delete

<213>Human

please insert

<221>

Partial Sequence Encoding Human IL-15

please move to section <223>

<300>

<308>NCBI pubmed Genbank Accession No. : U14407

same error

<309> ← pls insert

<400>3

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Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
1 5 10 15 20

ait gat gct act tta tat acg gaa agt gat gtt cac ccc agt tgc aaa gta aca gca atg 120
Ile Asp Ala Thr Leu Tyr Thr Glu Ser Asp Val His Pro Ser Cys Lys Val Thr Ala Met
25 30 35 40

aag tgc ttt etc ttg gag tta caa gtt att tca ctt gag tcc gga gat gca agt att cat 180
Lys Cys Phe Leu Leu Glu Leu Gln Val Ile Ser Leu Glu Ser Gly Asp Ala Ser Ile His
45 50 55 60

gat aca gta gaa aat ctg atc atc cta gca aac aac agt ttg tct tct aat ggg aat gta 240
Asp Thr Val Glu Asn Leu Ile Ile Leu Ala Asn Asn Ser Leu Ser Ser Asn Gly Asn Val
65 70 75 80

aca gaa tct gga tgc aaa gaa tgt gag gaa ctg gag gaa aaa aat att aaa gaa ttt ttg 300
Thr Glu Ser Gly Cys Lys Glu Cys Glu Glu Leu Glu Glu Lys Asn Ile Lys Glu Phe Leu
85 90 95 100

cag agt ttt gta cat att gtc caa atg ttc utc aac act tct 342
Gln Ser Phe Val His Ile Val Gln Met Phe Ile Asn Thr Ser
105 110
```

<210>4

<211>402

<212> mRNA and RT

<213> Artificial Chimeric Sequence

<220>

<221> IL-2SP/IL-15MP

<223> Artificial Chimeric Sequence Encoding IL-2SP/IL-15MP

<300>

<308>NCBI pubmed Genbank IL-2 Accession No. : V00564

IL-15 Accession No. : U14407

<309> ← insert

please insert
dates for each
accession No.

<400>4

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alg tac agg atg caa etc ctg tct tgc att gca cta agt ctt gca ctt gtc aca aac agt 60
Met Tyr Arg Met Gln Leu Leu Ser Cys Ile Ala Leu Ser Leu Ala Leu Val Thr Asn Ser
1 5 10 15 20
Sequence encoding IL-2signal peptide delete

aac tgg gtg aat gta ata agt gat ttg aaa aaa att gaa gat ctt att caa tct atg cat 120
Asn Trp Val Asn Val Ile Ser Asp Leu Lys Lys Ile Glu Asp Leu Ile Gln Ser Met His
25 30 35 40
```

att Ile	gat Asp	gct Ala	act Thr	tta Leu 45	tat Tyr	acg Thr	gaa Glu	agt Ser	gat Asp 50	ggt Val	cac His	ccc Pro	agt Ser	tgc Cys 55	aaa Lys	gta Val	aca Thr	gca Ala	atg Met 60	180
aag Lys	tgc Cys	ttt Phe	ctc Leu	ttg Leu 65	gag Glu	tta Leu	caa Gln	ggt Val	att Ile 70	tca Ser	ctt Leu	gag Glu	tcc Ser	gga Gly 75	gat Asp	gca Ala	agt Ser	att Ile	cat His 80	240
gat Asp	aca Thr	gta Val	gaa Glu	aat Asn 85	ctg Leu	atc Ile	atc Ile	cta Leu	gca Ala 90	aac Asn	aac Asn	agt Ser	ttg Leu	tct Ser 95	tct Ser	aat Asn	ggg Gly	aat Asn	gta Val 100	300
aca Thr	gaa Glu	tct Ser	gga Gly	tgc Cys 105	aaa Lys	gaa Glu	tgt Cys	gag Glu	gaa Glu 110	ctg Leu	gag Glu	gaa Glu	aaa Lys	aat Asn 115	att Ile	aaa Lys	gaa Glu	ttt Phe	ttg Leu 120	360
cag Gln	agt Ser	ttt Phe	gta Val	cat His 125	att Ile	gtc Val	caa Gln	atg Met	ttc Phe 130	atc Ile	aac Asn	act Thr	tct Ser	402						